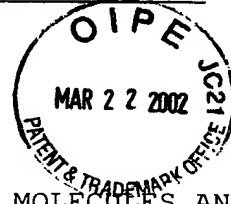


IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Mary Cismowski et al.
Serial No.: 09/709,103
Filed : November 8, 2000
For : AGS PROTEINS AND NUCLEIC ACID MOLECULES AND USES
THEREFOR



1185 Avenue of the Americas
New York, New York 10036
March 18, 2002

U.S. Patent and Trademark Office
Box Sequence, P.O. Box 2327
Arlington, VA 22202

Sir:

STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(e) attached hereto has the same information as the paper copy of the "Sequence Listing" submitted herewith as **Exhibit D** in connection with the above-identified application.

I hereby declare that all statements made herein are of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,

Joseph B. Crystal
Joseph B. Crystal
Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: The statement in accordance with 37 C.F.R. 1.821 (f) filed 3/22/02 does not include a statement of "no new matter". (see 37 CFR 1.821 (g)).

Applicant Must Provide:

- ☐ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY



SEQUENCE LISTING

<110> Cismowski, Mary
Duzic, Emir

<120> AGS Proteins and Nucleic Acid Molecules and Uses Therefor

<130> 60388-A-PCT-US

<140> 09/709,103

<141> 2000-11-08

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<170> PatentIn version 3.1

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Leu	Ser	Ile	Pro	Ala	Lys	Asn	Cys	Tyr	Arg	Met	Val	Ile	Leu	Gly	Ser	
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Thr Ile Glu Asp Phe His Arg Lys Phe Tyr Ser Ile Arg Gly Glu Val	
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Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
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Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
85 90 95

Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
100 105 110

Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
115 120 125

Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly
130 135 140

Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
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Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
165 170 175

Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe
180 185 190

Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys
195 200 205

Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn
210 215 220

Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Gly Asp Pro Gly
225 230 235 240

Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His
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<223> Xaa at position 4 may be any amino acid

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Leu Ala Ala Leu Pro His Ser Cys Leu Glu Arg Ala Lys Glu Ile Lys
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Ile Lys Leu Gly Ile Leu Leu Gln Lys Pro Asp Ser Val Gly Asp Leu
25 30 35

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Val Ile Pro Tyr Asn Glu Lys Pro Glu Lys Pro Ala Lys Thr Gln Lys
40 45 50

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Thr Ser Leu Asp Glu Ala Leu Gln Trp Arg Asp Ser Leu Asp Lys Leu
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70 75 80

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Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Ile Ala Cys Glu Asp Tyr
85 90 95 100

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Lys Lys Ile Lys Ser Pro Ala Lys Met Ala Glu Lys Ala Lys Gln Ile
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Tyr Glu Glu Phe Ile Gln Thr Glu Ala Pro Lys Glu Val Asn Ile Asp
120 125 130

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His Phe Thr Lys Asp Ile Thr Met Lys Asn Leu Val Glu Pro Ser Leu
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150 155 160

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Asp Ser Leu Pro Arg Phe Val Arg Ser Glu Phe Tyr Gln Glu Leu Ile
165 170 175 180

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Lys

ataaccctgc atttcccatt aatctacata tcttcccaca gcagctttgc tcagtgtac 697

ccacatggga aaaatcccag gggatgttgc ttactttttt tgcccacact gctttggata 757

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 gttaataaaa gtttataaga tttttatgaa gcagccactg tatgatattt taagcaaata 1117
 tgttatttaa aatattgatc cttcccttgg accacettca tgttagtgg gtattataaa 1177
 taagagatac aaccatgaat atattatggt tatacaaaat caatctgaac acaattcata 1237
 aagatttctc ttttatacct tctcactgg cccctccac ctgcccatag tcaccaaatt 1297
 ctgttttaaa tcaatgacct aagatcaaca atgaagtatt ttataaatgt atttatgctg 1357
 ctgactgtg ggtcaaagt ttccattttc aaattattta gaattcttat gagtttaaaa 1417
 tttgtaaatt tctaaatcca atcatgtaa atgaaactgt tgctccattg gagtagtctc 1477
 ccacctaaat atcaagatgg ctatatgcta aaaagagaaa atatggtcaa gtctaaaatg 1537
 gctaattgtc ctatgatgct attatcatag actaatgaca tttatcttca aaacaccaaa 1597
 ttgtctttag aaaaattaat gtgattacag gtagaggcct tctaggtgag acacttttaa 1657
 ggtacactgc attttgcaaa aaaaaaaaaa aaaa 1691

<210> 25

<211> 181

<212> PRT

<213> Homo Sapiens

<400> 25

Met Cys Lys Gly Leu Ala Ala Leu Pro His Ser Cys Leu Glu Arg Ala
 1 5 10 15

Lys Glu Ile Lys Ile Lys Leu Gly Ile Leu Leu Gln Lys Pro Asp Ser
 20 25 30

Val Gly Asp Leu Val Ile Pro Tyr Asn Glu Lys Pro Glu Lys Pro Ala
 35 40 45

Lys Thr Gln Lys Thr Ser Leu Asp Glu Ala Leu Gln Trp Arg Asp Ser
 50 55 60

Leu Asp Lys Leu Leu Gln Asn Asn Tyr Gly Leu Ala Ser Phe Lys Ser
 65 70 75 80

Phe Leu Lys Ser Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Ile Ala
 85 90 95

Cys Glu Asp Tyr Lys Lys Ile Lys Ser Pro Ala Lys Met Ala Glu Lys
100 105 110

Ala Lys Gln Ile Tyr Glu Glu Phe Ile Gln Thr Glu Ala Pro Lys Glu
115 120 125

Val Asn Ile Asp His Phe Thr Lys Asp Ile Thr Met Lys Asn Leu Val
130 135 140

Glu Pro Ser Leu Ser Ser Phe Asp Met Ala Gln Lys Arg Ile His Ala
145 150 155 160

Leu Met Glu Lys Asp Ser Leu Pro Arg Phe Val Arg Ser Glu Phe Tyr
165 170 175

Gln Glu Leu Ile Lys
180

<210> 26

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 26

ccagatctaa agatgccgat ttgggcg

27

<210> 27

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 27

ccccatggtt ttatatttgt tgtaaaaagt ag

32

<210> 28

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 28

cgggatccat gtgcaaaggg cttgcaggtc

30

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 29

ccgctcgagt taggcacact gagggacc

28

<210> 30

<211> 41

<212> DNA

<213> Homo Sapiens

<400> 30

agtcggtacc cgcataagatc tgcaggatgc cctttttgac g

41

<210> 31

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 31
gtacgtcgac ttgattttc agaaacttga tggc

34

<210> 32

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 32
tggcctcgag atgacaaatt caaaagaaga cg

32

<210> 33

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 33
atcactgcag ctatgctaca acattccaaa at

32

<210> 34

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 34
gggtcatgaa actggccgcg atgatcaaga ag

32

<210> 35

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 35

gatagtcgac ctagctgatg acgcagcgct c

31

<210> 36

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 36

cgcattgtca tcctcgtttc gtccaagggt g

31

<210> 37

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 37

ccaccttgga cgaaacgagg atgaccatgc g

31

<210> 38

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 38

ccaaggacaa ggagcgagc gtcacagct ag

32

<210> 39

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 39

ctagctgatg acgctgcgct ccttgctcctt gg

32

<210> 40

<211> 837

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (1) .. (834)

<223>

<400> 40

atg cct gct tct ctc gct ttg ttg cag ccc cga gcc atg atg aag act
Met Pro Ala Ser Leu Ala Leu Leu Gln Pro Arg Ala Met Met Lys Thr
1 5 10 15

48

ttg tcc agc ggg aac tgc acg ctc agt gtg ccc gcc aaa aac tca tac
Leu Ser Ser Gly Asn Cys Thr Leu Ser Val Pro Ala Lys Asn Ser Tyr
20 25 30

96

cgc atg gtg gtg ctg ggt gcc tct cgg gtg ggc aag agc tcc atc gtg
Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys Ser Ser Ile Val
35 40 45

144

tct cgc ttc ctc aat ggc cgc ttt gag gac cag tac aca ccc acc atc
Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr Thr Pro Thr Ile
50 55 60

192

gag gac ttc cac cgt aag gta tac aac atc cgc ggc gac atg tac cag Glu Asp Phe His Arg Lys Val Tyr Asn Ile Arg Gly Asp Met Tyr Gln 65 70 75 80	240
ctc gac atc ctg gat acc tct ggc aac cac ccc ttc ccc gcc atg cgc Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg 85 90 95	288
agg ctg tcc atc ctc aca ggg gat gtc ttc atc ctg gtg ttc agc ctg Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu 100 105 110	336
gat aac cgg gag tcc ttc gat gag gtc aag cgc ctt cag aag cag atc Asp Asn Arg Glu Ser Phe Asp Glu Val Lys Arg Leu Gln Lys Gln Ile 115 120 125	384
ctg gag gtc aag tcc tgc ctg aag aac aag acc aag gag gcg gcg gag Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Ala Ala Glu 130 135 140	432
ctg ccc atg gtc atc tgt ggc aac aag aac gac cac ggc gag ctg tgc Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His Gly Glu Leu Cys 145 150 155 160	480
cgc cag gtg ccc acc acc gag gcc gag ctg ctg gtg tcg ggc gac gag Arg Gln Val Pro Thr Glu Ala Glu Leu Leu Val Ser Gly Asp Glu 165 170 175	528
aac tgc gcc tac ttc gag gtg tcg gcc aag aag aac acc aac gtg gac Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn Thr Asn Val Asp 180 185 190	576
gag atg ttc tac gtg ctc ttc agc atg gcc aag ctg cca cac gag atg Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu Pro His Glu Met 195 200 205	624
agc ccc gcc ctg cat cgc aag atc tcc gtg cag tac ggt gac gcc ttc Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr Gly Asp Ala Phe 210 215 220	672
cac ccc agg ccc ttc tgc atg cgc cgc gtc aag gag atg gac gcc tat His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu Met Asp Ala Tyr 225 230 235 240	720
ggc atg gtc tcg ccc ttc gcc cgc cgc ccc agc gtc aac agt gac ctc Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val Asn Ser Asp Leu 245 250 255	768
aag tac atc aag gcc aag gtc ctt cgg gaa ggc cag gcc cgt gag agg Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln Ala Arg Glu Arg 260 265 270	816
gac aag tgc acc atc cag tga Asp Lys Cys Thr Ile Gln 275	837

<210> 41

<211> 278

<212> PRT

<213> Homo Sapiens

<400> 41

Met Pro Ala Ser Leu Ala Leu Leu Gln Pro Arg Ala Met Met Lys Thr
1 5 10 15

Leu Ser Ser Gly Asn Cys Thr Leu Ser Val Pro Ala Lys Asn Ser Tyr
20 25 30

Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys Ser Ser Ile Val
35 40 45

Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr Thr Pro Thr Ile
50 55 60

Glu Asp Phe His Arg Lys Val Tyr Asn Ile Arg Gly Asp Met Tyr Gln
65 70 75 80

Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg
85 90 95

Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu
100 105 110

Asp Asn Arg Glu Ser Phe Asp Glu Val Lys Arg Leu Gln Lys Gln Ile
115 120 125

Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Ala Ala Glu
130 135 140

Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His Gly Glu Leu Cys
145 150 155 160

Arg Gln Val Pro Thr Thr Glu Ala Glu Leu Leu Val Ser Gly Asp Glu
165 170 175

Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn Thr Asn Val Asp
180 185 190

Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu Pro His Glu Met
195 200 205

Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr Gly Asp Ala Phe
210 215 220

His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu Met Asp Ala Tyr
225 230 235 240

Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val Asn Ser Asp Leu
245 250 255

Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln Ala Arg Glu Arg
260 265 270

Asp Lys Cys Thr Ile Gln
275

<210> 42

<211> 15

<212> PRT

<213> Homo Sapiens

<400> 42

Asp Thr Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Asn Val Asp
1 5 10 15

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 43

ttctcgcgga tgtacatga

19

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Probe/Primer

<400> 44

tccaccgcaa gttctactcc

20

<210> 45

<211> 1740

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (146) .. (988)

<223>

<400> 45

gagcggagcc ggagcccaaa gcccgagccg cgcccagccc gagcagagcc ctccagccgc 60

tcaccccgcg tgccacccca ggcacctca gccgctctct gcccttctct cggcccgcg 120

cccgcctcg cggccctct gcca atg aaa ctg gcc gcg atg atc aag aag 172
Met Lys Leu Ala Ala Met Ile Lys Lys
1 5

atg tgc ccg agc gac tcg gag ctg agt atc ccg gcc aag aac tgc tat 220
Met Cys Pro Ser Asp Ser Glu Leu Ser Ile Pro Ala Lys Asn Cys Tyr
10 15 20 25

cgc atg gtc atc ctc ggc tcg tcc aag gtg ggc aag acg gcc atc gtg 268
Arg Met Val Ile Leu Gly Ser Ser Lys Val Gly Lys Thr Ala Ile Val
30 35 40

tcg cgc ttc ctc acc ggc cgc ttc gag gac gcc tac acg cct acc atc 316
Ser Arg Phe Leu Thr Gly Arg Phe Glu Asp Ala Tyr Thr Thr Ile
45 50 55

gag gac ttc cac cgc aag ttc tac tcc atc cgc ggc gag gtc tac cag 364
Glu Asp Phe His Arg Lys Phe Tyr Ser Ile Arg Gly Glu Val Tyr Gln
60 65 70

ctc gac atc ctc gac acg tcc ggc aac cac ccg ttc ccc gcc atg cgg 412
Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg
75 80 85

cgc ctc tcc atc ctc aca gga gac gtt ttc atc ctg gtg ttc agt ctg	460
Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu	
90 95 100 105	
gac aac cgc gac tcc ttc gag gag gtg cag cgg ctc agg cag cag atc	508
Asp Asn Arg Asp Ser Phe Glu Glu Val Gln Arg Leu Arg Gln Gln Ile	
110 115 120	
ctc gac acc aag tct tgc ctc aag aac aaa acc aag gag aac gtg gac	556
Leu Asp Thr Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Asn Val Asp	
125 130 135	
gtg ccc ctg gtc atc tgc ggc aac aag ggt gac cgc gac ttc tac cgc	604
Val Pro Leu Val Ile Cys Gly Asn Lys Gly Asp Arg Asp Phe Tyr Arg	
140 145 150	
gag gtg gac cag cgc gag atc gag cag ctg gtg ggc gac gac ccc cag	652
Glu Val Asp Gln Arg Glu Ile Glu Gln Leu Val Gly Asp Asp Pro Gln	
155 160 165	
cgc tgc gcc tac ttc gag atc tgc gcc aag aag aac agc agc ctg gac	700
Arg Cys Ala Tyr Phe Glu Ile Ser Ala Lys Lys Asn Ser Ser Leu Asp	
170 175 180 185	
cag atg ttc cgc gcg ctc ttc gcc atg gcc aag ctg ccc agc gag atg	748
Gln Met Phe Arg Ala Leu Phe Ala Met Ala Lys Leu Pro Ser Glu Met	
190 195 200	
agc cca gac ctg cac cgc aag gtc tgc gtg cag tac tgc gac gtg ctg	796
Ser Pro Asp Leu His Arg Lys Val Ser Val Gln Tyr Cys Asp Val Leu	
205 210 215	
cac aag aag gcg ctg cgg aac aag aag ctg ctg cgg gcc ggc agc ggc	844
His Lys Lys Ala Leu Arg Asn Lys Lys Leu Leu Arg Ala Gly Ser Gly	
220 225 230	
ggc ggc ggc ggc gac ccg ggc gac gcc ttt ggc atc gtg gca ccc ttc	892
Gly Gly Gly Gly Asp Pro Gly Asp Ala Phe Gly Ile Val Ala Pro Phe	
235 240 245	
gcg cgc cgg ccc agc gta cac agc gac ctc atg tac atc cgc gag aag	940
Ala Arg Arg Pro Ser Val His Ser Asp Leu Met Tyr Ile Arg Glu Lys	
250 255 260 265	
gcc agc gcc ggc agc cag gcc aag gac aag gag cgc tgc gtc atc agc	988
Ala Ser Ala Gly Ser Gln Ala Lys Asp Lys Glu Arg Cys Val Ile Ser	
270 275 280	
taggagcccc gccgcgtgg cgacacaacc taaggaggac ctttttggtta agtcaaattcc	1048
aacggccccgg tgcgccccag gccgggagcg cgcgaggact ggcgtctccc ctccggcgga	1108
tccgccccca gcaactgggga ggcgccactg aaccgagaag ggacgggcat ctgctccgga	1168
aggaaagaga acgggccaag actgggacta ttccccaccc ccggtccccc attgaggccc	1228
gccacccccca taactttggg agcgagggcc cagccgaggg tggattttatc ttctcaaaga	1288
cctaagagtg agcgcgggggt gggggaggga tgtgaagtta tccagcctct gctaggcttc	1348

aagaaaccgt catgcccgct tgagggtcag gacccacggg gcattatctt gtctgtgatt 1408
ccgggttgct gtgacagccg gtagagcctc tgcctcccg aaactaagcg ggggggctg 1468
ggtcaaataca tagccaagtg acttggttac atgtgagtga aactgcacaa aggaacacaa 1528
aacaaaactt gcactttaac ggtagtccg gtgtcaacat ggacacgaac aaaaccttac 1588
ccagggtgttt atactgtgtg tgtgtgaggt ctttaaagtt attgctttat ttgggttttt 1648
aatatacaat aaaataattt aaaatggaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1708
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1740

<210> 46

<211> 281

<212> PRT

<213> Homo Sapiens

<400> 46

Met Lys Leu Ala Ala Met Ile Lys Lys Met Cys Pro Ser Asp Ser Glu
1 5 10 15

Leu Ser Ile Pro Ala Lys Asn Cys Tyr Arg Met Val Ile Leu Gly Ser
20 25 30

Ser Lys Val Gly Lys Thr Ala Ile Val Ser Arg Phe Leu Thr Gly Arg
35 40 45

Phe Glu Asp Ala Tyr Thr Pro Thr Ile Glu Asp Phe His Arg Lys Phe
50 55 60

Tyr Ser Ile Arg Gly Glu Val Tyr Gln Leu Asp Ile Leu Asp Thr Ser
65 70 75 80

Gly Asn His Pro Phe Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly
85 90 95

Asp Val Phe Ile Leu Val Phe Ser Leu Asp Asn Arg Asp Ser Phe Glu
100 105 110

Glu Val Gln Arg Leu Arg Gln Gln Ile Leu Asp Thr Lys Ser Cys Leu
115 120 125

Lys Asn Lys Thr Lys Glu Asn Val Asp Val Pro Leu Val Ile Cys Gly
130 135 140

Asn Lys Gly Asp Arg Asp Phe Tyr Arg Glu Val Asp Gln Arg Glu Ile
145 150 155 160

Glu Gln Leu Val Gly Asp Asp Pro Gln Arg Cys Ala Tyr Phe Glu Ile
165 170 175

Ser Ala Lys Lys Asn Ser Ser Leu Asp Gln Met Phe Arg Ala Leu Phe
180 185 190

Ala Met Ala Lys Leu Pro Ser Glu Met Ser Pro Asp Leu His Arg Lys
195 200 205

Val Ser Val Gln Tyr Cys Asp Val Leu His Lys Lys Ala Leu Arg Asn
210 215 220

Lys Lys Leu Leu Arg Ala Gly Ser Gly Gly Gly Gly Asp Pro Gly
225 230 235 240

Asp Ala Phe Gly Ile Val Ala Pro Phe Ala Arg Arg Pro Ser Val His
245 250 255

Ser Asp Leu Met Tyr Ile Arg Glu Lys Ala Ser Ala Gly Ser Gln Ala
260 265 270

Lys Asp Lys Glu Arg Cys Val Ile Ser
275 280

<210> 47

<211> 189

<212> PRT

<213> Homo Sapiens

<400> 47

Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
1 5 10 15

Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20 25 30

Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35 40 45

Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50 55 60

Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65 70 75 80

Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
85 90 95

Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
100 105 110

Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
115 120 125

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
130 135 140

Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
145 150 155 160

Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
165 170 175

Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
180 185

<210> 48

<211> 206

<212> PRT

<213> Homo Sapiens

<400> 48

Met Ala Ala Asn Lys Pro Lys Gly Gln Asn Ser Leu Ala Leu His Lys
1 5 10 15

Val Ile Met Val Gly Ser Gly Gly Val Gly Lys Ser Ala Leu Thr Leu
20 25 30

Gln Phe Met Tyr Asp Glu Phe Val Glu Asp Tyr Glu Pro Thr Lys Ala
35 40 45

Asp Ser Tyr Arg Lys Lys Val Val Leu Asp Gly Glu Glu Val Gln Ile
50 55 60

Asp Ile Leu Asp Thr Ala Gly Gln Glu Asp Tyr Ala Ala Ile Arg Asp
65 70 75 80

Asn Tyr Phe Arg Ser Gly Glu Gly Phe Leu Cys Val Phe Ser Ile Thr
85 90 95

Glu Met Glu Ser Phe Ala Ala Thr Ala Asp Phe Arg Glu Gln Ile Leu
100 105 110

Arg Val Lys Glu Asp Glu Asn Val Pro Phe Leu Leu Val Gly Asn Lys
115 120 125

Ser Asp Leu Glu Asp Lys Arg Gln Val Ser Val Glu Glu Ala Lys Asn
130 135 140

Arg Ala Glu Gln Trp Asn Val Asn Tyr Val Glu Thr Ser Ala Lys Thr
145 150 155 160

Arg Ala Asn Val Asp Lys Val Phe Phe Asp Leu Met Arg Glu Ile Arg
165 170 175

Ala Arg Lys Met Glu Asp Ser Lys Glu Lys Asn Gly Lys Lys Lys Arg
180 185 190

Lys Ser Leu Ala Lys Arg Ile Arg Glu Arg Cys Cys Ile Leu
195 200 205

<210> 49

<211> 205

<212> PRT

<213> Homo Sapiens

<400> 49

Met Ser Ser Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu
1 5 10 15

Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala
20 25 30

Asp Asp Thr Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe
35 40 45

Lys Ile Arg Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys Leu Gln Ile
50 55 60

Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr
65 70 75 80

Tyr Arg Gly Ala His Gly Ile Ile Val Val Tyr Asp Val Thr Asp Gln
85 90 95

Glu Ser Phe Asn Asn Val Lys Gln Trp Leu Gln Glu Ile Asp Arg Tyr
100 105 110

Ala Ser Glu Asn Val Asn Lys Leu Leu Val Gly Asn Lys Cys Asp Leu
115 120 125

Thr Thr Lys Lys Val Val Asp Tyr Thr Thr Ala Lys Glu Phe Ala Asp
130 135 140

Ser Leu Gly Ile Pro Phe Leu Glu Thr Ser Ala Lys Asn Ala Thr Asn
145 150 155 160

Val Glu Gln Ser Phe Met Thr Met Ala Ala Glu Ile Lys Lys Arg Met
165 170 175

Gly Pro Gly Ala Thr Ala Gly Gly Ala Glu Lys Ser Asn Val Lys Ile
180 185 190

Gln Ser Thr Pro Val Lys Gln Ala Gly Gly Gly Cys Cys
195 200 205

<210> 50

<211> 210

<212> PRT

<213> Homo Sapiens

<400> 50

Met Thr Ala Ala Gln Ala Ala Gly Glu Glu Ala Pro Pro Gly Val Arg
1 5 10 15

Ser Val Lys Val Val Leu Val Gly Asp Gly Gly Cys Gly Lys Thr Ser
20 25 30

Leu Leu Met Val Phe Ala Asp Gly Ala Phe Pro Glu Ser Tyr Thr Pro
35 40 45

Thr Val Phe Glu Arg Tyr Met Val Asn Leu Gln Val Lys Gly Lys Pro
50 55 60

Val His Leu His Ile Trp Asp Thr Ala Gly Gln Asp Asp Tyr Asp Arg
65 70 75 80

Leu Arg Pro Leu Phe Tyr Pro Asp Ala Ser Val Leu Leu Leu Cys Phe
85 90 95

Asp Val Thr Ser Pro Asn Ser Phe Asp Asn Ile Phe Asn Arg Trp Tyr
100 105 110

Pro Glu Val Asn His Phe Cys Lys Lys Val Pro Ile Ile Val Val Gly
115 120 125

Cys Lys Thr Asp Leu Arg Lys Asp Lys Ser Leu Val Asn Lys Leu Arg
130 135 140

Arg Asn Gly Leu Glu Pro Val Thr Tyr His Arg Gly Gln Glu Met Ala
145 150 155 160

Arg Ser Val Gly Ala Val Ala Tyr Leu Glu Cys Ser Ala Arg Leu His
165 170 175

Asp Asn Val His Ala Val Phe Gln Glu Ala Ala Glu Val Ala Leu Ser
180 185 190

Ser Arg Gly Arg Asn Phe Trp Arg Arg Ile Thr Gln Gly Phe Cys Val
195 200 205

Val Thr
210

<210> 51

<211> 191

<212> PRT

<213> Homo Sapiens

<400> 51

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys
1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser Glu Tyr
20 25 30

Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile Gly Gly
35 40 45

Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr
50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Val
65 70 75 80

Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys Glu Lys
85 90 95

Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe Leu Leu
100 105 110

Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr Ile Glu Lys
115 120 125

Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr Ala Glu Lys
130 135 140

Leu Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys Ser Ala Leu
145 150 155 160

Thr Gln Arg Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu Ala Ala
165 170 175

Leu Glu Pro Pro Glu Thr Gln Pro Lys Arg Lys Cys Cys Ile Phe
180 185 190

<210> 52

<211> 192

<212> PRT

<213> Homo Sapiens

<400> 52

Met Gln Ala Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys
1 5 10 15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Ala Phe Pro Gly Glu Tyr
20 25 30

Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Ser
35 40 45

Lys Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr
50 55 60

Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile
65 70 75 80

Cys Phe Ser Leu Val Ser Pro Ala Ser Tyr Glu Asn Val Arg Ala Lys
85 90 95

Trp Phe Pro Glu Val Arg His His Cys Pro Ser Thr Pro Ile Ile Leu
100 105 110

Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys
115 120 125

Leu Lys Glu Lys Lys Leu Ala Pro Ile Thr Tyr Pro Gln Gly Leu Ala
130 135 140

Leu Ala Lys Glu Ile Asp Ser Val Lys Tyr Leu Glu Cys Ser Ala Leu
145 150 155 160

Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val
165 170 175

Leu Cys Pro Gln Pro Thr Arg Gln Gln Lys Arg Ala Cys Ser Leu Leu
180 185 190

<210> 53

<211> 181

<212> PRT

<213> Homo Sapiens

<400> 53

Met Gly Gly Phe Phe Ser Ser Ile Phe Ser Ser Leu Phe Gly Thr Arg
1 5 10 15

Glu Met Arg Ile Leu Ile Leu Gly Leu Asp Gly Ala Gly Lys Thr Thr
20 25 30

Ile Leu Tyr Arg Leu Gln Val Gly Glu Val Val Thr Thr Ile Pro Thr
35 40 45

Ile Gly Phe Asn Val Glu Thr Val Thr Tyr Lys Asn Leu Lys Phe Gln
50 55 60

Val Trp Asp Leu Gly Gly Gln Thr Ser Ile Arg Pro Tyr Trp Arg Cys
65 70 75 80

Tyr Tyr Ser Asn Thr Asp Ala Val Ile Tyr Val Val Asp Ser Cys Asp
85 90 95

Arg Asp Arg Ile Gly Ile Ser Lys Ser Glu Leu Val Ala Met Leu Glu
100 105 110

Glu Glu Glu Leu Arg Lys Ala Ile Leu Val Val Phe Ala Asn Lys Gln
115 120 125

Asp Met Glu Gln Ala Met Thr Ser Ser Glu Met Ala Asn Ser Leu Gly
130 135 140

Leu Pro Ala Leu Lys Asp Arg Lys Trp Gln Ile Phe Lys Thr Ser Ala
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Thr Lys Gly Thr Gly Leu Asp Glu Ala Met Glu Trp Leu Val Glu Thr
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Leu Lys Ser Arg Gln
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 35 40 45
 Phe Glu Ile Asp Thr Gln Arg Ile Glu Leu Ser Leu Trp Asp Thr Ser
 50 55 60
 Gly Ser Pro Tyr Tyr Asp Asn Val Arg Pro Leu Ser Tyr Pro Asp Ser
 65 70 75 80
 Asp Ala Val Leu Ile Cys Phe Asp Ile Ser Arg Pro Glu Thr Leu Asp
 85 90 95
 Ser Val Leu Lys Lys Trp Lys Gly Glu Ile Gln Glu Phe Cys Pro Asn
 100 105 110
 Thr Lys Met Leu Leu Val Gly Cys Lys Ser Asp Leu Arg Thr Asp Val
 115 120 125
 Ser Thr Leu Val Glu Leu Ser Asn His Arg Gln Thr Pro Val Ser Tyr
 130 135 140
 Asp Gln Gly Ala Asn Met Ala Lys Gln Ile Gly Ala Ala Thr Tyr Ile
 145 150 155 160
 Glu Cys Ser Ala Leu Gln Ser Glu Asn Ser Val Arg Asp Ile Phe His
 165 170 175
 Val Ala Thr Leu Ala Cys Val Asn Lys Thr Asn Lys Asn Val Lys Arg
 180 185 190
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 Ser Cys Thr Val Met
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<213> Artificial sequence

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